



SEQUENCE LISTING

<110> Salkoff, Lawrence
Schreiber, Matthew
Silvia, Chris
The Washington University
ICAgene Inc.

<120> A pH Sensitive Potassium Channel in Spermatocytes

<130> 018512-000120US

<140> 09/176,664

<141> 1998-10-21

<150> US 60/063,138

<151> 1997-10-22

<150> US 60/076,172

<151> 1998-02-27

<160> 53

<170> PatentIn Ver. 2.0

<210> 1

<211> 1112

<212> PRT

<213> Mus musculus

<220>

<223> mouse Slo3 (mSlo3)

<220>

<221> VARIANT

<222> (5)

<223> polymorphic variant #2 Leu -> Ile

<220>

<221> VARIANT

<222> (21)

<223> polymorphic variant #1 Ile -> Val

<220>

<221> VARIANT

<222> (25)

<223> polymorphic variant #3 Ala -> Ser

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Ala Thr Phe Phe Gly Gly Leu Ile Ile Leu Phe Leu Phe Arg Ile Ala
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Leu Lys Ser Ser Arg Ser Trp Lys Tyr Val Lys Gly Pro Arg Gly Leu
50 55 60

Leu Glu Leu Phe Ser Ser Arg Arg Ile Glu Ala Asn Pro Leu Arg Lys
 65 70 75 80
 Leu Tyr Phe His Gly Val Phe Arg Gln Arg Ile Glu Met Leu Leu Ser
 85 90 95
 Ala Gln Thr Val Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
 100 105 110
 Ser Ile Gly Ser Leu Val Ile Tyr Phe Ile Asn Ser Met Asp Pro Val
 115 120 125
 Arg Arg Cys Ser Ser Tyr Glu Asp Lys Ile Val His Gly Asp Leu Ser
 130 135 140
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Trp Ala Ala
 145 150 155 160
 Glu Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
 165 170 175
 Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp
 180 185 190
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Lys
 195 200 205
 Ile Leu Gln Ile Leu Gln Val Ile Lys Thr Ser Asn Ser Val Lys Leu
 210 215 220
 Ser Lys Leu Leu Ser Ile Val Ile Ser Thr Trp Phe Thr Ala Ala Gly
 225 230 235 240
 Phe Leu His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Asn Gly Arg
 245 250 255
 Asn Ser Gln Thr Met Ser Tyr Phe Glu Ser Ile Tyr Leu Val Thr Ala
 260 265 270
 Thr Met Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
 275 280 285
 Gly Arg Ile Phe Ile Val Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
 290 295 300
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ser Thr Arg Lys Lys
 305 310 315 320
 Tyr Thr Lys Pro Tyr Glu Ala Val Lys Gly Lys Lys Phe Ile Val Val
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 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe
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 Leu His Trp Lys Ser Gly Glu Ile Asn Ile Glu Ile Val Phe Leu Gly
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 Glu Thr Leu Pro Cys Leu Glu Leu Glu Thr Leu Leu Lys Cys His Thr
 370 375 380

Ser Cys Thr Asn Phe Val Cys Gly Thr Ala Leu Lys Phe Glu Asp Leu
 385 390 395 400
 Lys Arg Val Ala Val Glu Asn Ser Glu Ala Cys Leu Ile Leu Ala Asn
 405 410 415
 His Phe Cys Ser Asp Leu His Asp Glu Asp Asn Ser Asn Ile Met Arg
 420 425 430
 Val Leu Ser Ile Lys Asn Tyr Tyr Pro Gln Thr Arg Val Ile Ile Gln
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 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu
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 Thr Thr Leu Phe Ile Glu Gln Asn Gln Lys Val Phe Pro Lys His Pro
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 Trp Gln Lys His Phe Leu Asn Gly Leu Lys Asn Lys Ile Leu Thr Gln
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 Arg Leu Ser Asn Asp Phe Val Gly Met Thr Phe Pro Gln Val Ser Arg
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 Pro Phe Phe His Ser Cys Cys Thr Leu Ile Leu Asn Pro Ser Ser Gln
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 Val Arg Leu Asn Lys Asp Thr Leu Gly Phe Phe Ile Ala Asp Ser Ser
 580 585 590
 Lys Ala Val Lys Arg Ala Phe Phe Tyr Cys Ser Asn Cys His Ser Asp
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 Val Cys Asn Pro Glu Leu Ile Gly Lys Cys Asn Cys Lys Ile Lys Ser
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 675 680 685
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 690 695 700

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 740 745 750
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 Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile
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Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys
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Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe
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1060 1065 1070

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<212> DNA

<213> Mus musculus

<220>

<223> mouse Slo3 (mSlo3)

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atcttatttc	ttttcagaat	agccttgaaa	agctcaagaa	gttggaata	cgtcaagggg	180
ccaagaggac	tcttggaact	attctcatca	cgtagaatcg	aggctaattc	tttgaggaaa	240
ctttactttc	atggagtatt	tcgtcagcgc	atcgaaatgc	tgctttctgc	acagaccgtc	300
gtggggcaag	tggttggtgat	ccttgtcttt	gtactaagca	tcgggtctct	tgtgatctat	360
ttcatcaatt	caatggatcc	tggtcgaagg	tggtcttcat	atgaagacaa	aattgtccat	420
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tactgtttcca	actgtcacag	cgatgtgtgc	aatcctgagc	taattggaaa	gtgtaactgt	1860
aaaatcaaga	gccgacaaca	actcatagca	ccgaccatca	tggtgatgaa	aagcagcttg	1920
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cccttggaca aggtggttct gaaacgaagt gagaaggcaa aacacgagtt tcagaaccac 2160
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<210> 3
<211> 112
<212> PRT
<213> Homo sapiens

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<220>
<223> human Slo3-a (hSlo3-a)

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<222> (29)
<223> Xaa = any amino acid

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Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
 35                40                45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
 50                55                60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
 65                70                75                80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
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 <213> Homo sapiens

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 attatcttgg aactgttcac atcaggtacc atcgctagga gccatgtaag aagcctccac 180
 ttccagggac aatttcgtga tcatatagaa atgttgcttt cagcccagac ctttgtgggg 240
 caagtgttgg tgatccttgt ctttgtacta agcattgggt ctcttataat ctatttcac 300
 aattcwgctg accctgttgg aacgctgttc atcatatgaa gacaaaacca ttcctattga 360
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 <213> Mus musculus

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<210> 6
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 <212> PRT
 <213> Homo sapiens

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 <222> (29)
 <223> Xaa = any amino acid

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 Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
 35 40 45
 Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
 50 55 60
 Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
 65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
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Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val Gly Thr Leu Phe Ile Ile
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<212> PRT
<213> Homo sapiens

<220>
<223> human Slo3-c (hSLO3-c)

<220>
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<222> (29)
<223> Xaa = any amino acid

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20 25 30

Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
35 40 45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
50 55 60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
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Ile Tyr Phe Ile Asn Ser Met Asp Pro Val Gly Thr Leu Phe Ile Ile
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<210> 8
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 primer

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26

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 10
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 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 11
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 <213> Artificial Sequence

<220>
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<220>
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<210> 14
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<220>
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24

<210> 15
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<212> DNA
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24

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<213> Homo sapiens

<220>
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<220>
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<222> (6)
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<222> (25)
<223> polymorphic variant #3 Ala -> Ser

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35 40 45
Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile
50 55 60
Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser
65 70 75 80
Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser
85 90 95

Ala Gln Thr Phe Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
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 Ser Ile Gly Ser Leu Ile Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val
 115 120 125
 Gly Ser Cys Ser Ser Tyr Glu Asp Lys Thr Ile Pro Ile Asp Leu Val
 130 135 140
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Met Ala Ala
 145 150 155 160
 Asp Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
 165 170 175
 Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp
 180 185 190
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Gln
 195 200 205
 Ile Leu Gln Ile Leu Arg Ala Ile Lys Thr Ser Asn Ser Val Lys Phe
 210 215 220
 Ser Lys Leu Leu Ser Ile Ile Leu Ser Thr Trp Phe Thr Ala Ala Gly
 225 230 235 240
 Phe Ile His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Lys Gly Arg
 245 250 255
 Asn Ser Gln Asn Ile Ser Tyr Phe Glu Ser Ile Tyr Leu Val Met Ala
 260 265 270
 Thr Thr Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
 275 280 285
 Gly Arg Thr Phe Ile Met Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
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 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ala Asn Lys Arg Lys
 305 310 315 320
 Tyr Thr Ser Ser Tyr Glu Ala Leu Lys Gly Lys Lys Phe Ile Val Val
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 Glu Thr Pro Pro Ser Leu Glu Leu Glu Thr Ile Phe Lys Cys Tyr Leu
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 Ala Tyr Thr Thr Phe Ile Ser Gly Ser Ala Met Lys Trp Glu Asp Leu
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 Arg Arg Val Ala Val Glu Ser Ala Glu Ala Cys Leu Ile Ile Ala Asn
 405 410 415

Pro Leu Cys Ser Asp Ser His Ala Glu Asp Ile Ser Asn Ile Met Arg
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 Val Leu Ser Ile Lys Asn Tyr Asp Ser Thr Thr Arg Ile Ile Ile Gln
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 Ile Leu Gln Ser His Asn Lys Val Tyr Leu Pro Lys Ile Pro Ser Trp
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 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu
 485 490 495
 Thr Ser Leu Phe Val Glu Gln Asn Lys Lys Val Met Pro Lys Gln Thr
 500 505 510
 Trp Lys Lys His Phe Leu Asn Ser Met Lys Asn Lys Ile Leu Thr Gln
 515 520 525
 Arg Leu Ser Asp Asp Phe Ala Gly Met Ser Phe Pro Glu Val Ala Arg
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 545 550 555 560
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 565 570 575
 Gln Val Arg Ile Arg Lys Asn Thr Leu Gly Phe Phe Ile Ala Glu Thr
 580 585 590
 Pro Lys Asp Val Arg Arg Ala Leu Phe Tyr Cys Ser Val Cys His Asp
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 Asp Val Phe Ile Pro Glu Leu Ile Thr Asn Cys Gly Cys Lys Ser Arg
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 Ser Arg Gln His Ile Thr Val Pro Ser Val Lys Arg Met Lys Lys Cys
 625 630 635 640
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 Val Ser Ala Ser Thr Ser Ser Ile Ser Asn Phe Thr Thr Arg Thr Leu
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 675 680 685
 Phe His Trp Cys Lys Pro Thr Ser Leu Asp Lys Val Thr Leu Lys Arg
 690 695 700
 Thr Gly Lys Ser Lys Tyr Lys Phe Arg Asn His Ile Val Ala Cys Val
 705 710 715 720
 Phe Gly Asp Ala His Ser Ala Pro Met Gly Leu Arg Asn Phe Val Met
 725 730 735

Pro Leu Arg Ala Ser Asn Tyr Thr Arg Lys Glu Leu Lys Asp Ile Val
 740 745 750
 Phe Ile Gly Ser Leu Asp Tyr Leu Gln Arg Glu Trp Arg Phe Leu Arg
 755 760 765
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 770 775 780
 Asp Leu His Ala Ala Asn Ile Glu Gln Cys Ser Met Cys Ala Val Leu
 785 790 795 800
 Ser Pro Pro Pro Gln Pro Ser Ser Asn Gln Thr Leu Val Asp Thr Glu
 805 810 815
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 Ser Asp Pro Ser Pro Ser Val Ser Glu Glu Thr Pro Gly Tyr Thr Asn
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 Glu Gly Ser Leu Gln Glu Thr Asn Leu His Leu Ser Thr Ala Phe Ser
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Glu Ile Val Asn Lys Ala Ser Gln Thr Thr Glu Asp Thr Phe Arg His
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Lys Leu Ser Ser His Pro Leu Ile Gln Leu Leu Arg His Cys Ile His
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<212> PRT

<213> Homo sapiens

<220>

<223> human hSlo3-2 (hSlo3-2)

<400> 18

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Val Thr Phe Phe Ser Gly Leu Ile Ile Leu Leu Ile Phe Arg Leu Ile
    35                      40                      45

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Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile
    50                      55                      60

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Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser
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Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser
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Ala Gln Thr Phe Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
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Ser Ile Gly Ser Leu Ile Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val
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Gly Ser Cys Ser Ser Tyr Glu Asp Lys Thr Ile Pro Ile Asp Leu Val
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Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Met Ala Ala
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Asp Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
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 Ile Leu Gln Ile Leu Arg Ala Ile Lys Thr Ser Asn Ser Val Lys Phe
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 Ser Lys Leu Leu Ser Ile Ile Leu Ser Thr Trp Phe Thr Ala Ala Gly
 225 230 235 240
 Phe Ile His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Lys Gly Arg
 245 250 255
 Asn Ser Gln Asn Ile Ser Tyr Phe Glu Ser Ile Tyr Leu Val Met Ala
 260 265 270
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 275 280 285
 Gly Arg Thr Phe Ile Met Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
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 Ala Tyr Thr Thr Phe Ile Ser Gly Ser Ala Met Lys Trp Glu Asp Leu
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 485 490 495

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 Leu Gly Phe Phe Ile Ala Glu Thr Pro Lys Asp Val Arg Arg Ala Leu
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Phe	Leu	Asp	Ser	Leu	Leu	Ala	Thr	Ala	Phe	Tyr	Asn	Tyr	His	Val	Leu	
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His	Glu	Thr	Ile	Leu	Ser	Asp	Val	Asn	Pro	Arg	Asn	Thr	Phe	Gly	Gln	
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 Ala Gln Thr Val Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
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 Ser Ile Gly Ser Leu Val Ile Tyr Phe Ile Asn Ser Met Asp Pro Val
 115 120 125
 Arg Arg Cys Ser Ser Tyr Glu Asp Lys Ile Val His Gly Asp Leu Ser
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 260 265 270

Thr Met Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
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 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ser Thr Arg Lys Lys
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 Tyr Thr Lys Pro Tyr Glu Ala Val Lys Gly Lys Lys Phe Ile Val Val
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 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe
 340 345 350
 Leu His Trp Lys Ser Gly Glu Ile Asn Ile Glu Ile Val Phe Leu Gly
 355 360 365
 Glu Thr Leu Pro Cys Leu Glu Leu Glu Thr Leu Leu Lys Cys His Thr
 370 375 380
 Ser Cys Thr Asn Phe Val Cys Gly Thr Ala Leu Lys Phe Glu Asp Leu
 385 390 395 400
 Lys Arg Val Ala Val Glu Asn Ser Glu Ala Cys Leu Ile Leu Ala Asn
 405 410 415
 His Phe Cys Ser Asp Leu His Asp Glu Asp Asn Ser Asn Ile Met Arg
 420 425 430
 Val Leu Ser Ile Lys Asn Tyr Tyr Pro Gln Thr Arg Val Ile Ile Gln
 435 440 445
 Ile Leu Gln Ser Gln Asn Lys Val Phe Leu Ser Lys Ile Pro Asn Trp
 450 455 460
 Asp Trp Ser Ala Gly Asp Asn Ile Leu Cys Phe Ala Glu Leu Lys Leu
 465 470 475 480
 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu
 485 490 495
 Thr Thr Leu Phe Ile Glu Gln Asn Gln Lys Val Phe Pro Lys His Pro
 500 505 510
 Trp Gln Lys His Phe Leu Asn Gly Leu Lys Asn Lys Ile Leu Thr Gln
 515 520 525
 Arg Leu Ser Asn Asp Phe Val Gly Met Thr Phe Pro Gln Val Ser Arg
 530 535 540
 Leu Cys Phe Val Lys Leu Asn Leu Met Leu Ile Ala Ile Gln His Lys
 545 550 555 560
 Pro Phe Phe His Ser Cys Cys Thr Leu Ile Leu Asn Pro Ser Ser Gln
 565 570 575
 Val Arg Leu Asn Lys Asp Thr Leu Gly Phe Phe Ile Ala Asp Ser Ser
 580 585 590

Lys Ala Val Lys Arg Ala Phe Phe Tyr Cys Ser Asn Cys His Ser Asp
 595 600 605
 Val Cys Asn Pro Glu Leu Ile Gly Lys Cys Asn Cys Lys Ile Lys Ser
 610 615 620
 Arg Gln Gln Leu Ile Ala Pro Thr Ile Met Val Met Lys Ser Ser Leu
 625 630 635 640
 Thr Asp Phe Thr Thr Ser Ser His Ile His Ala Ser Met Ser Thr Glu
 645 650 655
 Ile His Thr Cys Phe Ser Arg Glu Gln Pro Ser Leu Ile Thr Ile Thr
 660 665 670
 Thr Asn Arg Pro Thr Thr Asn Asp Thr Val Asp Asp Thr Asp Met Leu
 675 680 685
 Asp Ser Ser Gly Met Phe His Trp Cys Arg Ala Met Pro Leu Asp Lys
 690 695 700
 Val Val Leu Lys Arg Ser Glu Lys Ala Lys His Glu Phe Gln Asn His
 705 710 715 720
 Ile Val Val Cys Val Phe Gly Asp Ala Gln Cys Thr Leu Val Gly Leu
 725 730 735
 Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr Arg Gln Glu
 740 745 750
 Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Glu Tyr Phe Gln Arg Glu
 755 760 765
 Trp Arg Phe Leu Arg Asn Phe Pro Lys Ile His Ile Met Pro Gly Ser
 770 775 780
 Ala Leu Tyr Met Gly Asp Leu Ile Ala Val Asn Val Glu Gln Cys Ser
 785 790 795 800
 Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile
 805 810 815
 Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Asn Ile Gln Ser Leu
 820 825 830
 Arg Ile Thr Ser Pro Thr Pro Gly Ser Ser Lys Ser Glu Val Lys Pro
 835 840 845
 Ser Ser Ala Phe Asp Ser Lys Glu Arg Lys Gln Arg Tyr Lys Gln Ile
 850 855 860
 Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu
 865 870 875 880
 Gln Met Gly Gly Leu Asp Gly Met Leu Lys Gly Thr Ser Leu His Leu
 885 890 895
 Ser Thr Ser Phe Ser Thr Gly Ala Val Phe Ser Asp Thr Phe Leu Asp
 900 905 910

Ser Leu Leu Ala Thr Ser Phe Tyr Asn Tyr His Val Val Glu Leu Leu
 915 920 925
 Gln Met Leu Val Thr Gly Gly Ile Ser Ser Glu Met Glu His Tyr Leu
 930 935 940
 Val Lys Glu Lys Pro Tyr Lys Thr Thr Asp Asp Tyr Glu Ala Ile Lys
 945 950 955 960
 Ser Gly Arg Thr Arg Cys Lys Leu Gly Leu Leu Ser Leu Asp Gln Thr
 965 970 975
 Val Leu Ser Gly Ile Asn Pro Arg Lys Thr Phe Gly Gln Leu Phe Cys
 980 985 990
 Gly Ser Leu Asp Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met
 995 1000 1005
 Ile Asp Glu Glu Glu Pro Ser Gln Glu His Lys Arg Phe Val Ile Thr
 1010 1015 1020
 Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys
 1025 1030 1035 1040
 Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe
 1045 1050 1055
 Asn Phe Arg Leu Lys Thr Thr Leu Gln Thr Arg Arg Arg His Trp Pro
 1060 1065 1070
 Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile
 1075 1080 1085
 Phe Thr Gln Ser Thr Thr Arg Glu Arg Gly Gly Leu Ser Thr Thr Thr
 1090 1095 1100
 Pro Glu Ser Ile Leu Trp Thr Arg Gln Leu Phe Cys Gly Ser Leu Asp
 1105 1110 1115 1120
 Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met Ile Asp
 1125 1130

<210> 21
 <211> 1236
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse Slol (mSlol)

<400> 21
 Met Asp Ala Leu Ile Ile Pro Val Thr Met Glu Val Pro Cys Asp Ser
 1 5 10 15
 Arg Gly Gln Arg Met Trp Trp Ala Phe Leu Ala Ser Ser Met Val Thr
 20 25 30
 Phe Phe Gly Gly Leu Phe Ile Ile Leu Leu Trp Arg Thr Leu Lys Tyr
 35 40 45

Leu Trp Thr Val Cys Cys His Cys Gly Gly Lys Thr Lys Glu Ala Gln
 50 55 60
 Lys Ile Asn Asn Gly Ser Ser Gln Ala Asp Gly Thr Leu Lys Pro Val
 65 70 75 80
 Asp Glu Lys Glu Glu Val Val Ala Ala Glu Val Gly Trp Met Thr Ser
 85 90 95
 Val Lys Asp Trp Ala Gly Val Met Ile Ser Ala Gln Thr Leu Thr Gly
 100 105 110
 Arg Val Leu Val Val Leu Val Phe Ala Leu Ser Ile Gly Ala Leu Val
 115 120 125
 Ile Tyr Phe Ile Asp Ser Ser Asn Pro Ile Glu Ser Cys Gln Asn Phe
 130 135 140
 Tyr Lys Asp Phe Thr Leu Gln Ile Asp Met Ala Phe Asn Val Phe Phe
 145 150 155 160
 Leu Leu Tyr Phe Gly Leu Arg Phe Ile Ala Ala Asn Asp Lys Leu Trp
 165 170 175
 Phe Trp Leu Glu Val Asn Ser Val Val Asp Phe Phe Thr Val Pro Pro
 180 185 190
 Val Phe Val Ser Val Tyr Leu Asn Arg Ser Trp Leu Gly Leu Arg Phe
 195 200 205
 Leu Arg Ala Leu Arg Leu Ile Gln Phe Ser Glu Ile Leu Gln Phe Leu
 210 215 220
 Asn Ile Leu Lys Thr Ser Asn Ser Ile Lys Leu Val Asn Leu Leu Ser
 225 230 235 240
 Ile Phe Ile Ser Thr Trp Leu Thr Ala Ala Gly Phe Ile His Leu Val
 245 250 255
 Glu Asn Ser Gly Asp Pro Trp Glu Asn Phe Gln Asn Asn Gln Ala Leu
 260 265 270
 Thr Tyr Trp Glu Cys Val Tyr Leu Leu Met Val Thr Met Ser Thr Val
 275 280 285
 Gly Tyr Gly Asp Val Tyr Ala Lys Thr Thr Leu Gly Arg Leu Phe Met
 290 295 300
 Val Phe Phe Ile Leu Gly Gly Leu Ala Met Phe Ala Ser Tyr Val Pro
 305 310 315 320
 Glu Ile Ile Glu Leu Ile Gly Asn Arg Lys Lys Tyr Gly Gly Ser Tyr
 325 330 335
 Ser Ala Val Ser Gly Arg Lys His Ile Val Val Cys Gly His Ile Thr
 340 345 350
 Leu Glu Ser Val Ser Asn Phe Leu Lys Asp Phe Leu His Lys Asp Arg
 355 360 365

Asp	Asp	Val	Asn	Val	Glu	Ile	Val	Phe	Leu	His	Asn	Ile	Ser	Pro	Asn		
370						375					380						
Leu	Glu	Leu	Glu	Ala	Leu	Phe	Lys	Arg	His	Phe	Thr	Gln	Val	Glu	Phe		
385					390					395					400		
Tyr	Gln	Gly	Ser	Val	Leu	Asn	Pro	His	Asp	Leu	Ala	Arg	Val	Lys	Ile		
				405					410					415			
Glu	Ser	Ala	Asp	Ala	Cys	Leu	Ile	Leu	Ala	Asn	Lys	Tyr	Cys	Ala	Asp		
			420					425					430				
Pro	Asp	Ala	Glu	Asp	Ala	Ser	Asn	Ile	Met	Arg	Val	Ile	Ser	Ile	Lys		
	435						440					445					
Asn	Tyr	His	Pro	Lys	Ile	Arg	Ile	Ile	Thr	Gln	Met	Leu	Gln	Tyr	His		
450						455					460						
Asn	Lys	Ala	His	Leu	Leu	Asn	Ile	Pro	Ser	Trp	Asn	Trp	Lys	Glu	Gly		
465					470					475					480		
Asp	Asp	Ala	Ile	Cys	Leu	Ala	Glu	Leu	Lys	Leu	Gly	Phe	Ile	Ala	Gln		
				485					490					495			
Ser	Cys	Leu	Ala	Gln	Gly	Leu	Ser	Thr	Met	Leu	Ala	Asn	Leu	Phe	Ser		
			500					505					510				
Met	Arg	Ser	Phe	Ile	Lys	Ile	Glu	Glu	Asp	Thr	Trp	Gln	Lys	Tyr	Tyr		
	515						520					525					
Leu	Glu	Gly	Val	Ser	Asn	Glu	Met	Tyr	Thr	Glu	Tyr	Leu	Ser	Ser	Ala		
530						535					540						
Phe	Val	Gly	Leu	Ser	Phe	Pro	Thr	Val	Cys	Glu	Leu	Cys	Phe	Val	Lys		
545					550					555					560		
Leu	Lys	Leu	Leu	Met	Ile	Ala	Ile	Glu	Tyr	Lys	Ser	Ala	Asn	Arg	Glu		
				565					570					575			
Ser	Arg	Ile	Leu	Ile	Asn	Pro	Gly	Asn	His	Leu	Lys	Ile	Gln	Glu	Gly		
		580						585					590				
Thr	Leu	Gly	Phe	Phe	Ile	Ala	Ser	Asp	Ala	Lys	Glu	Val	Lys	Arg	Ala		
	595					600						605					
Phe	Phe	Tyr	Cys	Lys	Ala	Cys	His	Asp	Asp	Val	Thr	Asp	Pro	Lys	Arg		
610						615					620						
Ile	Lys	Lys	Cys	Gly	Cys	Arg	Arg	Leu	Ile	Tyr	Phe	Glu	Asp	Glu	Gln		
625					630					635					640		
Pro	Pro	Thr	Leu	Ser	Pro	Lys	Lys	Lys	Gln	Arg	Asn	Gly	Gly	Met	Arg		
			645						650					655			
Asn	Ser	Pro	Asn	Thr	Ser	Pro	Lys	Leu	Met	Arg	His	Asp	Pro	Leu	Leu		
			660					665					670				
Ile	Pro	Gly	Asn	Asp	Gln	Ile	Asp	Asn	Met	Asp	Ser	Asn	Val	Lys	Lys		
		675					680					685					

Tyr	Asp	Ser	Thr	Gly	Met	Phe	His	Trp	Cys	Ala	Pro	Lys	Glu	Ile	Glu	690	695	700
Lys	Val	Ile	Leu	Thr	Arg	Ser	Glu	Ala	Ala	Met	Thr	Val	Leu	Ser	Gly	705	710	715
His	Val	Val	Val	Cys	Ile	Phe	Gly	Asp	Val	Ser	Ser	Ala	Leu	Ile	Gly	725	730	735
Leu	Arg	Asn	Leu	Val	Met	Pro	Leu	Arg	Ala	Ser	Asn	Phe	His	Tyr	His	740	745	750
Glu	Leu	Lys	His	Ile	Val	Phe	Val	Gly	Ser	Ile	Glu	Tyr	Leu	Lys	Arg	755	760	765
Glu	Trp	Glu	Thr	Leu	His	Asn	Phe	Pro	Lys	Val	Ser	Ile	Leu	Pro	Gly	770	775	780
Thr	Pro	Leu	Ser	Arg	Ala	Asp	Leu	Arg	Ala	Val	Asn	Ile	Asn	Leu	Cys	785	790	795
Asp	Met	Cys	Val	Ile	Leu	Ser	Ala	Asn	Gln	Asn	Asn	Ile	Asp	Asp	Thr	805	810	815
Ser	Leu	Gln	Asp	Lys	Glu	Cys	Ile	Leu	Ala	Ser	Leu	Asn	Ile	Lys	Ser	820	825	830
Met	Gln	Phe	Asp	Asp	Ser	Ile	Gly	Val	Leu	Gln	Ala	Asn	Ser	Gln	Gly	835	840	845
Phe	Thr	Pro	Pro	Gly	Met	Asp	Arg	Ser	Ser	Pro	Asp	Asn	Ser	Pro	Val	850	855	860
His	Gly	Met	Leu	Arg	Gln	Pro	Ser	Ile	Thr	Thr	Gly	Val	Asn	Ile	Pro	865	870	875
Ile	Ile	Thr	Glu	Leu	Val	Asn	Asp	Thr	Asn	Val	Gln	Phe	Leu	Asp	Gln	885	890	895
Asp	Asp	Asp	Asp	Asp	Pro	Asp	Thr	Glu	Leu	Tyr	Leu	Thr	Gln	Pro	Phe	900	905	910
Ala	Cys	Gly	Thr	Ala	Phe	Ala	Val	Ser	Val	Leu	Asp	Ser	Leu	Met	Ser	915	920	925
Ala	Thr	Tyr	Phe	Asn	Asp	Asn	Ile	Leu	Thr	Leu	Ile	Arg	Thr	Leu	Val	930	935	940
Thr	Gly	Gly	Ala	Thr	Pro	Glu	Leu	Glu	Ala	Leu	Ile	Ala	Glu	Glu	Asn	945	950	955
Ala	Leu	Arg	Gly	Gly	Tyr	Ser	Thr	Pro	Gln	Thr	Leu	Ala	Asn	Arg	Asp	965	970	975
Arg	Cys	Arg	Val	Ala	Gln	Leu	Ala	Leu	Leu	Asp	Gly	Pro	Phe	Ala	Asp	980	985	990
Leu	Gly	Asp	Gly	Gly	Cys	Tyr	Gly	Asp	Leu	Phe	Cys	Lys	Ala	Leu	Lys	995	1000	1005

Thr Tyr Asn Met Leu Cys Phe Gly Ile Tyr Arg Leu Arg Asp Ala His
 1010 1015 1020
 Leu Ser Thr Pro Ser Gln Cys Thr Lys Arg Tyr Val Ile Thr Asn Pro
 1025 1030 1035 1040
 Pro Tyr Glu Phe Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met
 1045 1050 1055
 Gln Phe Asp His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser
 1060 1065 1070
 Ser His Ser Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser
 1075 1080 1085
 Ile Pro Ser Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser
 1090 1095 1100
 Arg Asp Lys Gln Asn Ala Thr Arg Met Thr Arg Met Gly Gln Ala Glu
 1105 1110 1115 1120
 Lys Lys Trp Phe Thr Asp Glu Pro Asp Asn Ala Tyr Pro Arg Asn Ile
 1125 1130 1135
 Gln Ile Lys Pro Met Ser Thr His Met Ala Asn Gln Ile Asn Gln Tyr
 1140 1145 1150
 Lys Ser Thr Ser Ser Leu Ile Pro Pro Ile Arg Glu Val Glu Asp Glu
 1155 1160 1165
 Cys Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met Gln Phe Asp
 1170 1175 1180
 His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser Ser His Ser
 1185 1190 1195 1200
 Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser Ile Pro Ser
 1205 1210 1215
 Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser Arg Asp Lys
 1220 1225 1230
 Gln Asn Ala Thr
 1235

<210> 22
 <211> 1262
 <212> PRT
 <213> Drosophila sp.

<220>
 <223> Drosophila Slol (dSlol)

<400> 22
 Met Ala Ser Gly Leu Ile Asp Thr Asn Phe Ser Ser Thr Leu Ala Asn
 1 5 10 15
 Gly Met Ser Gly Cys Asp Gln Ser Thr Val Glu Pro Leu Ala Asp Asp
 20 25 30

Pro Thr Asp Ser Pro Phe Asp Ala Asp Asp Cys Leu Lys Val Arg Lys
 35 40 45
 Tyr Trp Cys Phe Leu Leu Ser Ser Ile Phe Thr Phe Leu Ala Gly Leu
 50 55 60
 Leu Val Val Leu Leu Trp Arg Ala Phe Ala Phe Val Ser Cys Arg Lys
 65 70 75 80
 Glu Pro Asp Leu Gly Pro Asn Asp Pro Lys Gln Lys Glu Gln Lys Ala
 85 90 95
 Ser Arg Asn Lys Gln Glu Phe Glu Gly Thr Phe Met Thr Glu Ala Lys
 100 105 110
 Asp Trp Ala Gly Glu Leu Ile Ser Gly Gln Thr Thr Thr Gly Arg Ile
 115 120 125
 Leu Val Val Leu Val Phe Ile Leu Ser Ile Ala Ser Leu Ile Ile Tyr
 130 135 140
 Phe Val Asp Ala Ser Ser Glu Glu Val Glu Arg Cys Gln Lys Trp Ser
 145 150 155 160
 Asn Asn Ile Thr Gln Gln Ile Asp Leu Ala Phe Asn Ile Phe Phe Met
 165 170 175
 Val Tyr Phe Phe Ile Arg Phe Ile Ala Ala Ser Asp Lys Leu Trp Phe
 180 185 190
 Met Leu Glu Met Tyr Ser Phe Val Asp Tyr Phe Thr Ile Pro Pro Ser
 195 200 205
 Phe Val Ser Ile Tyr Leu Asp Arg Thr Trp Ile Gly Leu Arg Phe Leu
 210 215 220
 Arg Ala Leu Arg Leu Met Thr Val Pro Asp Ile Leu Gln Tyr Leu Asn
 225 230 235 240
 Val Leu Lys Thr Ser Ser Ser Ile Arg Leu Ala Gln Leu Val Ser Ile
 245 250 255
 Phe Ile Ser Val Trp Leu Thr Ala Ala Gly Ile Ile His Leu Leu Glu
 260 265 270
 Asn Ser Gly Asp Pro Leu Asp Phe Asn Asn Ala His Arg Leu Ser Tyr
 275 280 285
 Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly Tyr
 290 295 300
 Gly Asp Val Tyr Cys Glu Thr Val Leu Gly Arg Thr Phe Leu Val Phe
 305 310 315 320
 Phe Leu Leu Val Gly Leu Ala Val Phe Ala Ser Trp Ile Pro Glu Ile
 325 330 335
 Thr Glu Leu Ala Ala Gln Arg Ser Lys Tyr Gly Gly Thr Tyr Ser Lys
 340 345 350

Asp Pro Arg Lys Arg His Ile Val Val Cys Gly His Ile Thr Tyr Glu
 355 360 365
 Ser Val Ser His Phe Leu Lys Asp Phe Leu His Glu Asp Arg Glu Asp
 370 375 380
 Val Asp Val Glu Val Val Phe Leu His Arg Lys Pro Pro Asp Leu Glu
 385 390 395 400
 Leu Glu Gly Leu Phe Lys Arg His Phe Thr Thr Val Glu Phe Phe Gln
 405 410 415
 Gly Thr Ile Met Asn Pro Ile Asp Leu Gln Arg Val Lys Val His Glu
 420 425 430
 Ala Asp Ala Cys Leu Val Leu Ala Asn Lys Tyr Cys Gln Asp Pro Asp
 435 440 445
 Ala Glu Asp Ala Ala Asn Ile Met Arg Val Ile Ser Ile Lys Asn Tyr
 450 455 460
 Ser Asp Asp Ile Arg Val Ile Ile Gln Leu Met Gln Tyr His Asn Lys
 465 470 475 480
 Ala Tyr Leu Leu Asn Ile Pro Ser Trp Asp Trp Lys Gln Gly Asp Asp
 485 490 495
 Val Ile Cys Leu Ala Glu Leu Lys Leu Gly Phe Ile Ala Gln Ser Cys
 500 505 510
 Leu Ala Pro Gly Phe Ser Thr Met Met Ala Asn Leu Phe Ala Met Arg
 515 520 525
 Ser Phe Lys Thr Ser Pro Asp Met Gln Ser Trp Thr Asn Asp Tyr Leu
 530 535 540
 Arg Gly Thr Gly Met Glu Met Tyr Thr Glu Thr Leu Ser Pro Thr Phe
 545 550 555 560
 Ile Gly Ile Pro Phe Ala Gln Ala Thr Glu Leu Cys Phe Ser Lys Leu
 565 570 575
 Lys Leu Leu Leu Leu Ala Ile Glu Ile Lys Gly Ala Glu Glu Gly Ala
 580 585 590
 Asp Ser Lys Ile Ser Ile Asn Pro Arg Gly Ala Lys Ile Gln Ala Asn
 595 600 605
 Thr Gln Gly Phe Phe Ile Ala Gln Ser Ala Asp Glu Val Lys Arg Ala
 610 615 620
 Trp Phe Tyr Cys Lys Ala Cys His Glu Asp Ile Lys Asp Glu Thr Leu
 625 630 635 640
 Ile Lys Lys Cys Lys Cys Lys Asn Leu Thr Val Gln Pro Arg Ser Lys
 645 650 655
 Phe Asp Asp Leu Gly Asp Ile Thr Arg Asp Arg Glu Asp Thr Asn Leu
 660 665 670

Leu Asn Arg Asn Val Arg Arg Pro Asn Gly Thr Gly Asn Gly Thr Gly
 675 680 685
 Gly Met His His Met Asn Ser Thr Arg Ala Ala Ala Ala Ala Ala
 690 695 700
 Ala Ala Gly Lys Gln Val Asn Lys Val Lys Pro Thr Val Asn Val Ser
 705 710 715 720
 Arg Gln Val Glu Gly Gln Val Ile Ser Pro Ser Gln Tyr Asn Arg Pro
 725 730 735
 Thr Ser Arg Ser Ser Gly Thr Gly Thr Gln Asn Gln Asn Gly Gly Val
 740 745 750
 Ser Leu Pro Ala Gly Ile Ala Asp Asp Gln Ser Lys Asp Phe Asp Phe
 755 760 765
 Glu Lys Thr Glu Met Lys Tyr Asp Ser Thr Gly Met Phe His Trp Ser
 770 775 780
 Pro Ala Lys Ser Leu Gln Asp Cys Ile Leu Asp Arg Asn Gln Ala Ala
 785 790 795 800
 Met Thr Val Leu Asn Gly His Val Val Val Cys Leu Phe Ala Asp Pro
 805 810 815
 Asp Ser Pro Leu Ile Gly Leu Arg Asn Leu Val Met Pro Leu Arg Ala
 820 825 830
 Ser Asn Phe His Tyr His Glu Leu Lys His Val Val Ile Val Gly Ser
 835 840 845
 Val Asp Tyr Ile Arg Arg Glu Trp Lys Met Leu Gln Asn Leu Pro Lys
 850 855 860
 Ile Ser Val Leu Asn Gly Ser Pro Leu Ser Arg Ala Asp Leu Arg Ala
 865 870 875 880
 Val Asn Val Asn Leu Cys Asp Met Cys Cys Ile Leu Ser Ala Lys Val
 885 890 895
 Pro Ser Asn Asp Asp Pro Thr Leu Ala Asp Lys Glu Ala Ile Leu Ala
 900 905 910
 Ser Leu Asn Ile Lys Ala Met Thr Phe Asp Asp Thr Ile Gly Val Leu
 915 920 925
 Ser Gln Arg Gly Pro Glu Phe Asp Asn Leu Ser Ala Thr Ala Gly Ser
 930 935 940
 Pro Ile Val Leu Gln Arg Arg Gly Ser Val Tyr Gly Ala Asn Val Pro
 945 950 955 960
 Met Ile Thr Glu Leu Val Asn Asp Gly Asn Val Gln Phe Leu Asp Gln
 965 970 975
 Asp Asp Asp Asp Asp Pro Asp Thr Glu Leu Tyr Leu Thr Gln Pro Phe
 980 985 990

Ala Cys Gly Thr Ala Phe Ala Val Ser Val Leu Asp Ser Leu Met Ser
995 1000 1005

Thr Thr Tyr Phe Asn Gln Asn Ala Leu Thr Leu Ile Arg Ser Leu Ile
1010 1015 1020

Thr Gly Gly Ala Thr Pro Glu Leu Glu Leu Ile Leu Ala Glu Gly Ala
1025 1030 1035 1040

Gly Leu Arg Gly Gly Tyr Ser Thr Val Glu Ser Leu Ser Asn Arg Asp
1045 1050 1055

Arg Cys Arg Val Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln
1060 1065 1070

Phe Gly Glu Cys Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys
1075 1080 1085

Ser Tyr Gly Met Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser
1090 1095 1100

Ser Ser Cys Asp Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro
1105 1110 1115 1120

Asp Asp Phe Ser Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln
1125 1130 1135

Phe Asp Pro Gly Leu Glu Tyr Lys Pro Pro Ala Val Arg Ala Pro Ala
1140 1145 1150

Gly Gly Arg Gly Thr Asn Thr Gln Gly Ser Gly Val Gly Gly Gly Gly
1155 1160 1165

Ser Asn Lys Asp Asp Asn Ser Leu Ser Asn Arg Asp Arg Cys Arg Val
1170 1175 1180

Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln Phe Gly Glu Cys
1185 1190 1195 1200

Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys Ser Tyr Gly Met
1205 1210 1215

Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser Ser Ser Cys Asp
1220 1225 1230

Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro Asp Asp Phe Ser
1235 1240 1245

Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln Phe Asp
1250 1255 1260

<210> 23

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:sense
oligonucleotide

<400> 23
 gtggatgata ccgacatgct ggac 24

<210> 24
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:antisense
 oligonucleotide

<400> 24
 gagaccacct ctctcccgtg tcgt 24

<210> 25
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mSlo3 (S4 to
 S5) sense primer

<400> 25
 ctcgaactcc ctaaaatctt acagat 26

<210> 26
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mSlo3 (S4 to
 S5) antisense primer

<400> 26
 ttccgttgag ccaggggtca ccagaatt 28

<210> 27
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mSlo3 (S8 to
 S9) sense primer

<400> 27
 tctgctttgt gaagctaaat ct 22

<210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mSlo3 (S8 to S9) antisense primer

 <400> 28
 tttcaaagcc tcttttagcgg taa 23

 <210> 29
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:mSlo3 (S9 to S10) sense primer

 <400> 29
 ttatgcctgg atctgcactc tacatg 26

 <210> 30
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:mSlo3 (S9 to S10) antisense primer

 <400> 30
 atagtttccg tctactaccg aaa 23

 <210> 31
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:control human beta-actin sense primer

 <400> 31
 gatgatatcg ccgcgctcgt cgtcgac 27

 <210> 32
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:control human beta-actin antisense primer

 <400> 32
 tcggtccagg tctgcgtcct accgtac 27

<210> 33
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:northern blot
 sense primer

 <400> 33
 cggaacgctc atgtacaatc gaaatcca 28

 <210> 34
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:northern blot
 antisense primer

 <400> 34
 ttccgttgag ccaggggtca ccagaatt 28

 <210> 35
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human testis
 cDNA library primer

 <400> 35
 ggacgcgctc attctttcct cctt 24

 <210> 36
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human testis
 cDNA library primer

 <400> 36
 tgcccaaaac ctcaacccaa aata 24

 <210> 37
 <211> 4
 <212> PRT
 <213> Mus musculus

 <220>
 <221> PEPTIDE
 <222> (1)..(4)
 <223> mSlo3 Region A peptide starting at amino acid 792

<400> 37
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<210> 38
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<210> 42
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<210> 43
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Val Asn Asp Thr
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<210> 44
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<400> 44
Gly Thr Ala Phe
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<210> 45
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<213> Artificial Sequence

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and mSlo3 sequences at C-terminal end of chimera
Region B fragment

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<210> 46
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<210> 47
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<400> 47
Ser Glu Met Glu
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<210> 48
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<400> 48
Thr Gln Pro Phe
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<210> 49
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Pro Glu Leu Glu
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<210> 50
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<210> 51
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His Leu Leu Pro
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Glu Leu Glu Ala
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a/ <400> 53
Glu Leu Val Pro
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